

STIC-Biotech/ChemLib

61261

From: Borin, Michael
Sent: Tuesday, February 26, 2002 1:59 PM
To: STIC-Biotech/ChemLib
Subject: Search request: 09/540325

Examiner: M.Borin
CM1 12A01
AU: 1631; Mailbox 12D01

Tel.: 305-4506

RE: 09/5403²³⁵~~25~~; cyanidium nucl. acids

CRFE

Please conduct search of polynucleotide SEQ ID 1 against the commercial and interference databases.

Thank you

Searcher: Paula Sheppard
Phone: 308-4499
Location: _____
Date Picked Up: 3/02/02
Date Completed: 3/04/04
Searcher Prep/Review: 10
Clerical: _____
Online time: 5

TYPE OF SEARCH:

NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

[illegible]

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VERSION	AF370158.1	GI:11877790		

KEYWORDS	FLI_CDNA.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana

REFERENCE
1 (bases 1 to 729)
Yamada, K., Liu, S.-X., Sakano, H., Pham, P. K., Banh, T., Chung, M. K.,
AUTHORS

TITLE	Full Length cDNA of gene T16K5.260/AT3g49910 (GI:67223436)
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 729)
AUTHORS	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,

TITLE Direct Submission
JOURNAL Submitted (18-APR-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the

collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PEGC (SSP) Consortium members carried out the sequencing and annotation of the RATL cDNAs: Yamada, K., Liu, S.X., Sakano, H., Pham, P. K., Bahh, J., Chung, M. K., Goldsmith, A.D., Lee, J.M., Quach, H. L., Tang, C.C., Tortiliani, M., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlén-Neumann, G., Kim, C., Kosegawa, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C. J., Shin, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A. Yamada, K. (SSP/PEGC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PEGC) contributed equally to this work as PIs.

FEATURES

SOURCE

gene

5'UTR

CDS

3, U

mis

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Matches 195;	Conservative	0;	Mismatches 118;	Indels 0;	Gaps 0;					

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ATF3A4				
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DEFINITION	Arabidopsis thaliana DNA chromosome 3, BAC clone F3A4.			
ACCESSION	AL132978			
VERSION	AL132978.1	GI:6434211		
KEYWORDS	.			
SOURCE	thale cress.			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 108158)			
AUTHORS	Barques,M., Collado,M.C., Navarro,P., Terol,J., Perez-Alonso,M., Mewes,H.W., Lemcke,K., Mayer,K.F.X., Queller,F. and Salanoubat,M.			
JOURNAL	Mewes,H.W., Lemcke,K., Mayer,K.F.X., Queller,F. and Salanoubat,M. unpublished			
REFERENCE	2 (bases 1 to 108158)			
AUTHORS	EU Arabidopsis sequencing, project.			
TITLE	Direct Submissions			
JOURNAL	Submitted (01-DEC-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopfersplitz 18a, D-82152 Martinsried, FRG. E-mail: lemcke@mbp.biochem.mpg.de, mayer@mbp.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Queller, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE, 2 rue Gaston Cremlieux, BP191, 91006 Evry Cedex, France; http://www.genoscope.cns.fr			

COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ .
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SNGLEFESVREVERERESDEPVAENPVRQIDELFOLLEINEGSDSDGVIADBG
EEEDFPMAGQEVONLHGKAKDIELEKTNVPAIDILKNSDVADKEEVDIAHAHVR
TVEYENFDNENEDFVELTEESSDESEKHDCETIVSYSNLNLPEK11AAESAROK

Query Match      30.4%; Score 124.2; DB 8; Length 108158;
Best Local Similarity 62.3%; Pred. No. 1e-22;
Matches 195; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 96 atgaagatccaagtgtatcgtctagagaagaagcagaggaacatacttcaa 155
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1631 ATGAAGTACAAACCAAGAGTACCTCTTCGCAGAAAGAACAGAGCATATTTCACA 1690
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QY 156 gaccactctctgtagcgaatactcatgtagtcacccctgtcagaagaactagtcg 215
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1691 GCTTCTCCAGGAGAGGCGGTGTGTAATGACCTCTCTCTCCACCGATCTTGTCAG 1750
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 216 aaatacagcgttcgtcttaccattcgaaaaagaagaagaatatactgtcgcga 275
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1751 AAGTACATGTCAGATCCATGCGGTAAGACGACGAGAGTTCAGTTCGTGCGT 1810
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 276 gcttcaaggttagagaagaagaattacaacgtgttatcgaagaataatcgcatacat 335
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1811 ACTTACAAAGGACGTGAAGGCGCAAGTTGTTTACCGTCGCAAAATGGGTGATTCAC 1870
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 336 atcgagaagtgacgaagaagaagaatgaatgaatgtaacctgtgtggataatcatca 395
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Db 1871 ATCGAGACATATCAGGAGGAGAGTGAATGACCAACCGTAACGTTGGGATTCACGCG 1930
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 396 tctaattgttgta 408
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1931 TCGAAAGTTGTGA 1943
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 5
YSP972HB/c YSP972HB 11941 bp DNA PLN 06-FEB-1999
LOCUS DEFINITION DB3993 Schizosaccharomyces pombe (strain 972h-) DNA, clone_1lb:Mizukami
ACCESSION D83993 Schizosaccharomyces pombe (strain 972h-) DNA, clone_1lb:Mizukami
VERSION D83993.1 GI:1236271 Schizosaccharomyces pombe (strain 972h-) DNA, clone_1lb:Mizukami
KEYWORD Schizosaccharomyces pombe (strain 972h-) DNA, clone_1lb:Mizukami
SOURCE Schizosaccharomyces pombe (strain 972h-) DNA, clone_1lb:Mizukami
ORGANISM Schizosaccharomyces pombe (strain 972h-) DNA, clone_1lb:Mizukami
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.

REFERENCE
AUTHORS 1 (bases 1 to 11941)
TITLE Yanagida,M.
JOURNAL Direct Submission
Submitted (12-MAR-1996) to the DDBJ/EMBL/GenBank databases.
Mitsunori Yanagida, Kyoto University, Department of Biophysics;
Kitsuhira-kawa-Oiwakecho, Sakyo-ku, Kyoto, Kyoto 606, Japan
(E-mail: kateyama@koto.biophys.kyoto-u.ac.jp, Tel:075-753-4205,
Fax:075-753-4208)
2 (sites)
REFERENCE
AUTHORS Kohnosu,A., Niwa,O., Yano,M., Saitoh,S., Katayama,T., Nagao,K. and
TITLE Mitsunori Yanagida, Kyoto University, Department of Biophysics;
JOURNAL Kitsuhira-kawa-Oiwakecho, Sakyo-ku, Kyoto, Kyoto 606, Japan
FEATURES
source Unpublished (1996)
Location/Qualifiers
1..11941
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="II"
/clone="cosmid 1228"
/map="2L between centromere and cdc2"
/complement(3855..4235)
/note="putative ribosomal protein 126, most similar to
pir: s51347 (68.6% identity in 121 aa overlap)"
/protein_id="BA12196.1"
/db_xref="GI:1236272"
/translation="MKFSRDVYSSRRKQKRAHFGAPSSVRYLMSAPLSKELEQYKI
RSIPVRDDITVIRGSKNGKRGKIRSVRRKFLILIEHVTREKAGAPVGTASK
VVITKLHDKRDLIVRGKQKVE"
/complement(5033..6739)
/note="similar to pir: s52731 (23.4% identity in 273 aa
overlap)"
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SWQSGYISGFEVNPVNSQYISITGLACEYFEERSLASVAVLQSTSEDMX
IYATDNEFGKVAEPNVPVNEGFIIDEVILPEYVTKNKSVAVALQSTSEDMX
TTPYSEVPYLDNRNGXSXSIDIDTVKPPVIGKPRVGGTTLPLNQTIGVADWF
RWNTNLNATVYHFNPSNPMQMLPISKEFNPDMPTYSSTYLHFNQVJONITTEPAAR
KRSILTAIRSLGDKRTIVLIGNGEDDLOIYBMAACPERILGFIIRVMSDFGVL
KXATXSXSLDEPVQYKPPATSTPDTPLKEFTTLKVDNEGASEFYQLEKPDVPS
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CN"
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/translation="MGFDVAGYLQSYSLKDWIRIIVYGVYMLXRPYLMKLGAKIOER
EHRKSLSEGVDTGLDPEMTHTGKPKPEHEEFTDDDEEENPDADFNGYSARRIRK
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/note="unnamed protein product"
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/db_xref="GI:1236275"
/translation="MSNSTEADLOLHTKNEHEKRRHSPVSKSDPPDAVVOGDNKNE
FYOSPCKMDVLELSDIDALTPPRAMQYPLKPPENNPHTGSALLHRYLDTNMO
VQYTPREPKNLDSOEYMDIDSSFPSPSTISKMPSLINDNSSHAUSLFAEEHES
YDSINPSGMSPEKTIQFSPHTMGVSSQDANERSLSLQRLTTLNDSNDSVYKEEDSW
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9526..10236
/note="unnamed protein product"
/codon_start=1
/protein_id="BA12200.1"
/db_xref="GI:1827510"
/translation="MSSIFGENIVSDSIYNNMELAXPDNTTTHPIYTNXXKGVQOE
SIXVSKETIDSTXSISLIGNIOXXMKALXKXIFKRLGVKATDLGFSNEHDDSDSLQ
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CDS		<p>TAAAGSYVPLKKAIGSSSEPVNSNLVTJDETMTDGDPEFLISVRRELFMGSPNSXXX XKHKEKLDPGPRYLXLRRAISVDENRKRELSPSDPVEIESYVINGELSNOKYEIV EISEBQNDPPAGYSQYL"</p> <p>/note="unnamed protein product" /codon_start=1 /protein_id="BA12201.1" /db_xref="GI:1827511" /translation="MARXRKTRGPSCGRRESCLTXHGLDPIKNLEITNLSIYPBV FSKSVNTKLRLTSSELPIAFKSGTYDGEGASVCNESCESSLBNPKSVALPENT" 10774..11364 /note="unnamed protein product" /codon_start=1 /protein_id="BA12202.1" /db_xref="GI:1827512" /translation="MLSLAKTRERADXXWSEEERTNYTNELLNPCKELCFHDSEF PHOQDLIMKYLAEFSAESILDELINLMMKOVFSKGHKLIVMPISPHCVQRPDD LVGVNSTAEFXSVDELTFTYDINTKILXTAPSPQAQMWLFIMHLHEITYGLFPPIX AHLDKOYSLLDYAKSVHRHPBELCTYQKCLEQSRI"</p>					
CDS							
BASE COUNT	3774 a	2224 c	2065 g	3755 t	123 others		
ORIGIN							
Query Match	28.9%	Score 117.8;	DB 8;	Length 11941;			
Best Local Similarity	61.0%;	Pred. No.	6.4e-21;				
Matches 191; Conservative	0;	Mismatches 122;	Indels 0;	Gaps 0;			
Qy	96	atgaagattacgtcaaaagttagtctgcgtcctaagaagaacgaggaagaacgatctttcaa	155				
Dd	4235	ATGAAGTTCCTCAGGAGATGTCACTAAGCTCGTGCCACAGAGAAGAGCTCACTTCGGC	4176				
Qy	156	gcaccatctcttcgtacgaagaataactcatgaigtgaccccttgccaagaactacgctcg	215				
Dd	4175	GCCCCCTCATCTGNAACGCCGCTGTATTATGTCCTGCCTCTTCCAAAGAGACTTAGAGAG	4116				
Qy	216	aataacagcgctgtcttcttacctattggaaaagaagcgaagtatcatagttgcgcga	275				
Dd	4115	CAATAACAAGATCCGTTCTCTTCCACTGTCGCTGATGACCAATACACTGTCAATCCGTG	4056				
Oy	276	gcttcaagggttagaagaagaagtltacaacglttatcgaagaagaatatcgatacat	335				
Dd	4055	TCCAACAAGAGTCCGGAAGCGAAGTAACACTCCGCTACCGTAAGAAGTCTCTTCTTT	3996				
Qy	336	atcgaagagatgacacagaagaacggaatgtaactgactgactcgttggaatacatcca	395				
Dd	3995	ATTGAGCGTGTGCACCCGCGAGAGGCCAACAGGTGCGCTGTGCACCOCGTCGTGATGACGCC	3936				
Qy	396	tctaagtgttgtta 408					
Dd	3935	TCTAAGTTGTCTCA 3923					
RESULT 6							
SPEC29B5/C	LOCUS	SPEC29B5	14147 bp	DNA	PLN	29-AUG-2000	
DEFINITION	S.pombe chromosome II cosmid C29B5.						
VERSION	AL391603						
KEYWORDS	AL391603.1 GI:9929282 60s ribosomal protein L26; atf1; isp4; sexual differentiation; transcription factor. fission yeast. Schizosaccharomyces pombe Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes. 1 (bases 1 to 14147) Wood,V., Rajandream,M.A., Barrell,B.G., Saunders,D. and Harris,D. Direct Submission Submitted (24-AUG-1999) European Schizosaccharomycetes genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk						
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT	Details of yeast sequencing at the Sanger Centre are available on						

the World Wide Web.
(URL: <http://www.sanger.ac.uk/Projects/S-pombe/>)
During 1995 to 1996 about 66% of *S. pombe* chromosome 1 was sequenced by the Sanger Centre. The sequencing of the *S. pombe* genome is now being continued with funding from The European Commission. Fourteen European sequencing laboratories, including the Sanger Centre, are participating in the project.
Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in Pombase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct splice donor/acceptor sites.
CDS are numbered using the following system eg SPBC25H2.01c, SP (S. pombe), B (chromosome 2), c25h2 (cosmid name), .01 (first CDS), c (complementary strand).
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring sublibraries.
Cosmid c29B5 is overlapped at the 3' end by cosmid c27, EMBL entry SPBC27, accession number AJ355866.

FEATURES
source
1. .14147
/organism="Schizosaccharomyces pombe"
/strain="972h-"
/db_xref="taxon:4896"
/chromosome="II"
/clone="cosmid c29B5"
/map="IIL"
1. .101
/note="nominal overlap with SPBC83 S. pombe chromosome 2"
224. .1924
/gene="atfi"
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224. .1924
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/note="SPBC29B5.01, len:567"
/codon_start=1
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/product="transcription factor atfi"
/protein_id="CAC05510.1"
/db_xref="GI:9953813"
/translation="MSPSPVNTSTEPASVAVNSGNATASSTOVPENNOSDFAPPSVSGOQOOSTIAPNGAGSVANANPADODSDGTPFVSLKLDEPNPFESFGSTAVGQVSLNRNPSLNSIPVGPAPAFATLLPVSIAIPDLISGAPGIAISPGAPWAWAFTRTMNPILSPATYDATTLPDYDNLNNSDASAARFSSGGFTGVNVEPFSLLTPWAGPAPSPGTANLILGFTPTDPSODPPDQRYRTFPROCKPVVNGTNGDSDYGCANAAVGLCLISQVPPDOOQKLQDPISSBNDQASTTANNLKQOQOOPFPIISPTQMNPPAVATGTMPNQASTTQOQPMYFMGSDQFNGMPSVYGVNVPADPSLLTRQTTDFSGMAVNGSTLPORTNSIDMPTANSPMYKLENTDVTSTSEPSNANNOSSPSSINGRASSSSANGSYSGKSRNSKNETDEEKRKSLERNRQAALCQRKKQWLNLQAKVEFYNNELTSLAQVSAALREIYISKTLILAHKDCPAKNSAAVATSVIGSDILAQRIMLG"

misc-feature
1658. .1825
/gene="atfi"
/note="Match to PF00170 bZIP, bZIP transcription factor Score 48.62"
complement(2997. .5354)
/gene="isp4"
/note="SPBC29B5.02c"
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/note="SPBC29B5.02c, len:786"
/codon_start=1
/label="isp4"
/product="sexual differentiation process protein isp4"
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	Best Local Similarity	61.0%;	Pred. NO. 6.2e-21;		
	Matches 191;	Conservative	0;	Mismatches 122;	Indels 0;
				Gaps	0;
Qy	96 atgaagattccaaaagttgtatcgctcgtactagaagaacgcagagaaacatactttcaa	155			
Db	11183 ATGAAGTTCCTCAGGAGGAGTACTAGCTCTGCTGGCAAGAGAAAGGCTACTCTTCGGC	11124			
Yy	156 gcaccattcttcgtacgacataactatagttgtcaaccccttgcacaaagaactactacg	215			

RESULT	7
LOCUS	AC091511
DEFINITION	AC091511 97911 bp DNA INV 09-JUN-2001 Leishmania major chromosome 35 clone P860 strain Friedlin, complete sequence.
ACCESSION	AC091511
VERSION	AC091511.2 GI:14333935
KEYWORDS	HTG.
SOURCE	Leishmania major.
ORGANISM	Leishmania major

Query Match	27.0%	Score 110.2	DB 3	Length 97911
Best Local Similarity	61.8%	Pred. No. 5.1e-19		
Matches 175: Conservative	0	Matches 108	Indels 0	Gaps 0
BASE COUNT	21394 a	27908 c	27877 g	20732 t
ORIGIN	/organism="Leishmania major" /strain="Friedlin" /db_xref="taxon:5664" /chromosome="35" /clone="P860"			

Accession	Sequence	Position
Oy 123	tcgagaagaagacagaggaagacgactactcttcaagcaccatctctgtacagcaatc	182
Dh 66203	TCCCGCCCAAGGCCCGCCCGCCGACCTTTAAGGCCCGGAGCATTGCGCCGTGCTC	66262
Oy 183	atgagtcacccctgtgccaaagaaactaagtaagaatacagcgtctcgtcttactcatt	242
Dh 66263	ATGAGCCGCCGCTCTCCAAAGAGACTGGCGCCCAAGTACAACTGCGTCGCATCCCGTG	66322
Oy 243	cgaagaagaagacgaatcatcatgctcgagagcttccaaggtatagaagaagaatc	302
Dh 66323	CGCAAGGCGACGAGGTATGTGTGAAGCGGCGCCCTTTCAAGGGCCGTGAGGGAAGGTG	66382

QY 303 accccggttatcgaaagaatcggatcatcatcagagagtgccaaagaanaagc 352
 |||||
 Db 66383 ACGGCGTCATCCGCCCTCAAGTGGGCTATCTCTATGCTAAAGTGAAACCGAGAAAGCG 66442
 |||||
 QY 363 aatggaatgaatgaactctgfyggaataatcaatcaatg 405
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 Db 66443 AAGGCTTCACCGGCGCGTGGGATCCATCCATCCCTCCAACTCG 66485
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RESULT	8		
CNS061DT			
LOCUS			
DEFINITION			
	CNS061DT	979 bp	DNA
	T7 end of clone ASOAO1906 of library ASOAO from strain CLIB 533		STS
	of <i>Saccharomyces bayanus</i> , sequence tagged site.		

ACCESSION	AL400167
VERSION	AL400167.1
SEQUENCE	GI:12155716

ORGANISM

REFERENCE

TITLE

JOURNAL
FEBBS Lett. 487 (1), 37-41 (2000)
PUBMED
11152880

REFERENCE
AUTHORS

TITLE Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies(1)
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)

TITLE	Genoscope - Centre National de Séquençage,
JOURNAL	Submitted (07-SEP-2000)
COMMENT	2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : serrefgenoscope.cns.fr - Web : www.genoscope.cns.fr) This SNS is part of a random genomic sequencing program of thirteen Genoscope - Centre National de Séquençage

yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pholia scabipolpha*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
source

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organism="Saccharomyces bayanus"  
strain="CLIB 533"  
variety="ivarum"  
db_xref="taxon:4931"  
clone="ASDAAD19H06"  
clone_1lb="ASOA"  
note="end : T"  
<528 : >887 :  
misc_feature
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BASE COUNT	337 a	168 c	186 g	286 t	2 others
ORIGIN					

Query Match	26.9%;	Score 109.8;	DB 11;	Length 979;
Best Local Similarity	60.0%;	Pred. No. 1.1e-18;		
Matches 183;	Conservative	0;	Mismatches 122;	Indels 0;
				Gaps 0.

QY	104	ttccaaagltglatcgttcgtctagaaagacagaggaagaacatcttctaagcacatc	163
Db	518	TTTTAATGAGCTCTCTCTGACAAACAAAGGCCAGAAAGGCTCACTTCAGCGCCCATC	5777
QY	164	ttctgtagcagaatctcatcgtatgtagaccctgttccaagaactacgtacgaatacag	2233
Db	578	CTCTCAACGTGTGTTTTGATGTCTGCTCCATTATCCAAAGAAATTGAGACTCATATCGG	6373
QY	224	cgttcgtctcttacctatctcgaagaagaagacgaatcatcagtttcgcyagccttcaa	2833
Db	638	TATCAAGCTTTGGCCATTCACAACAGAAAGATGAAGTCTTGCTGTGCTGGCTCCAGAA	6977
QY	284	gggtagagaagaaagttcacacgltgltatcgaagaataatctcgatatcatatcagag	3433
Db	698	GGGTCAACAAAGGTAAAGATTTCTTGTGTTTACAGATTGAAGTTGCTTTCAAGTTGCAA	7577
QY	344	agttaccagagaaaaaggaatgaaatgactcgtacccgttggaatatacatcatctaatgt	4033
Db	758	GGTCCCAAGGAAAAGGTCAACGGTCTTCCGTTCCAATCACTTGCACCAACCATTAAGT	8177
QY	404	tgtta	408
Db	818	TGTTA	822

	RESULT	9					25-JAN-2001
AX073298	LOCUS	AY073298	1348 bp	DNA	PAT		
	DEFINITION	Sequence 409 from Patent WO0102550.					
ACCESSION		AY073298					
VERSION		AY073298.1		GI:12563444			

ORGANISM *Candida albicans*
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes
Saccharomycetales; mitosporic Saccharomycetales; *Candida*.
REFERENCE 1 (bases 1 to 1348)

TITLE Cell death related drug targets in yeast and fungi
JOURNAL Patent: WO 0102550-A 409 11-JAN-2001;
JANSSEN PHARMACEUTICA N.V. (BE)

```

FEATURES
source
Location/Qualifiers
1. .1348
/username="Gardida alhicansa"

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BASE COUNT	512 a	194 c	196 g	446 t
ORIGIN				

Query Match	26.9%;	Score 109.8;	DB 6;	Length 1348;	.
Best Local Similarity	60.0%;	Pred. No. 1e-18;			
Matches 183;	Conservative	0;	Mismatches 122;	Indels 0;	Gaps 0

[illegible]

QY	344	agttaccagagaaaaagcggaatgtaatgactctgaactctgtgggaataacatccatctaatgt	403
Db	1216	ATTTCACAAAAGAAAATCAATATGTCCTTCTGTCCAAATCAACATTCATCTTAAAGT	1275
QY	404	tgttta	408
Db	1276	TGTCA	1280

RESULT	10			
LOCUS	CNS01B90			
DEFINITION	CNS01B90	480 bp	mRNA	02-SEP-1999
ACCESSION	U01139			
VERSION	U01139.1			
KEYWORDS	Botrytis cinerea strain T4	CDNA library	under conditions of	
SOURCE	Botrytis cinerea	nitrogen deprivation.		
ORGANISM	Botrytis cinerea	CDNA library; nitrogen deprivation.		
	Botryocinia fuckeliana			

REFERENCE
AUTHORS
TITLE
JOURNAL
1 (bases 1 to 480)
Bilton, F., Lewis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr
78026 Versailles, France
2 (bases 1 to 480)
Genoscope.
Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Séquençage

COMMENT

The cDNA library to be analyzed within the framework of this project was created using a *Botrytis cinerea* strain which was grown under conditions of nitrogen deprivation, which is the normal situation for *B. cinerea* during its development on its host plant. The library was produced in an oriented direction, in the pSII vector.

FEATURES	Location/Qualifiers
source	1. .480

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/organism="Notycolinia fuchkeliana"
/strain="T4"
/db_xref="taxon:40559"
/notes="genoscope sequence ID : W24h111"
BASE COUNT      132 a      128 c      116 g      104 t
      ORIGIN

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Query Match	26.1%;	Score 106.6;	DB 8;	Length 480;
Best Local Similarity	60.6%;	Pred. No. 8.1e-18;		
Matches 175; Conservative	0;	Mismatches 114;	Indels 0;	Gaps 0;

DY 120 tcgtctagaagaaacgacgaaggaaacatacttcaagcaccatcttcgtcagcagata 179
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 38 TCCTCCAGGAGAAAGTCCCGCAAGGCTCATTTGCATGCCCATTCACGGTCAGACGCTACC 97

QY 180 ctcaatgagtgcacccctgtgccaaagaaactacgttacgaataacagcgttcgttctaact 239
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98 ATCATGAGCGCTTCCTTTGACGAAGAAGTCCGTGAGAAAGTACAACAGTCCGGCTCATTCCA 15

240 atcgaagaagacgaagtaatacatagttcgcgaagcttccaaggtagagaaggaana
158 ATCAGAAGGATGATGAGTCCACCATCGTTCGTTCACACAAGGGCTCCGAGGGGAAG 217

QY 300 gttacaacgttgttatacgaagaataatcgcgatatcatatcgagagagtgcaccagaaaaa 359
+ + + + +
218 ATCACTCCGTCACCGTCAATATAGTCGTCCACGTCGAGCGTGTCGTAACGAGAAG 277
+ + + + +

2Y 360 gcgaatggaatgactgttacctgttgggaatacacatcataatgttcta 408
 1 |||| | | | | | | | | | | | | | | | |
 Db 278 TCCTCTGACAAATCCGTTCCCTCGGTATCCACCACATCCAAAGTCATCA 326

RESULT	11
CNS01CFH	
LOCUS	CNS01CFH 506 bp mRNA PIN
DEFINITION	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ACCESSION	U175461

VERSION ALL15461.1 GI:5830080
 KEYWORDS cDNA library; nitrogen deprivation.
 SOURCE Botryotinia fuckeliana.
 ORGANISM Botryotinia fuckeliana

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 506)
Bittori, P., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr
76026 Versailles, France
2 (bases 1 to 506)
Genoscope.
Direct Submission
Submitted (01-SEP-1999) Genoscope - Centre National de Sequences

COMMENT

The cDNA library to be analyzed within the framework of this project was created using a *Boltylis cinerea* strain which was grown under conditions of nitrogen deprivation, which is the normal situation for *B. cinerea* during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.

FEATURES	Location/Qualifiers
source	1. .506

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/organism="Botryotinia fuckeliana"
/strain="74"
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/note="Genoscope sequence ID : W54A061"
140 a 138 c 119 g 109 t
BASE COUNT
ORIGIN

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Query Match	26.1%	Score 106.6;	DB 8;	Length 506;
Best Local Similarity	60.6%;	Pred. No. 8e-18;		
Matches 175; Conservative	0;	Mismatches 114;	Indels 0;	Gaps 0

Oy 120 tcgctagagaagaacgaggaagaacacttctcaagcacaccatcttcgtacgaagaata 179
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TCCTCCAGAGAAGTCCCCGACAGGCTCATTTGGATGCCCATTCACGGGTGAGACGTACC 120

Qy 180 ctcacgagtgatgcacccttgtccaaagaactacgtacgaatacagctlgtcttaact 239
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Db 121 atcattagaggcgctcccttttagacgaagaactctcgtgagaagttaacaacgctccatcca 180

[illegible]

360 ggcgaatgaaactgactgtggtggaataacacatcaatgttatta 408
241 ATCACCCTCCGCTACCGCTGCAATTAACGTGTCCACGTGGACCTGTGTGTAAGGAAAG 300
Db

Db 301 TCCTGGACATCGTTCCTCGTATCAACCCATCCAAAGTCATCA 349

LOCUS	CNS019172	540 bp	mRNA	PLN	02-SEP-1999
DEFINITION	Botrytis cinerea strain T4 cDNA library under conditions of				
	nitrogen deprivation.				
ACCESSION	AL111303				
VERSION	AL111303.1	GI:5825922			
KEYWORDS	cDNA library; nitrogen deprivation.				

[illegible]

REFERENCE	2 (bases 1 to 540)
Genoscope.	
TITLE	Direct Submission
AUTHORS	Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage ; CP 5706 91057 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
JOURNAL	
COMMENT	<p>- Web : www.genoscope.cns.fr</p> <p>The cDNA library to be analyzed within the framework of this project was created using a <i>Botrytis cinerea</i> strain which was grown under conditions of nitrogen deprivation, which is the normal situation for <i>B. cinerea</i> during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.</p>
FEATURES	
source	<p>Location/Qualifiers</p> <p>1..540</p> <p>/organism="Botrytislina fuckeliana"</p> <p>/strain="T4"</p> <p>/db_xref="taxon:40559"</p> <p>/note="Genoscope sequence ID : W34H091"</p>
BASE COUNT	145 a 148 c 130 g 117 t
ORIGIN	
Query Match	26.1% Score 106.6; DB 8; Length 540;
Best Local Similarity	60.6% Pred. No. 8e-18;
Matches 175; Conservative 0; Mismatches 114; Indels 0; Gaps 0;	
QY 120	tcgtctagaagaacagacagagaagacatacttcaagcacatcttctgtacagcgata 179
Db 64	TCCTCCAGAGAGAAATCCCGCAGAGGCTCATTTGCGATGCCCATCAGCGTACAGCAACC 123
QY 180	ccacagagagacccctgtcccaaggaactacgtacgaataacacagcttcgtcttacct 239
Db 124	ATCATAGCGCGCTCTTTGACAGAGAACTCCGTGAGAGTACAAAGCTCCGCTCCATCCA 183
QY 240	attcgaagaagaacagaaagtaatactacagctcgtcggagcttcaagggtgagaagaaaa 299
Db 184	ATCAGAAAGATGATGAGAGGTACACATCGTCTGCTTCCAAAGGGCTCCGAGGGAAG 243
QY 300	gttacaacgtgttatcgaagaagaataatcgsataatcgaagaagatcaccagagaanaa 359
Db 244	ATCACCCTCGCTTACCCTGTTCAAATATCGTCGTCACACGTCGAGCGTGTCAAGGAGAG 303
QY 360	ggcgaatgcagtactgtacctgtggaatacatcatcatatgttgtta 408
Db 304	TCTCTTGGAACATCCGCTTCCCTCGGTATCCACCATCAAGGATCATCA 352
RESULT 14	
CNS01A0A	
LOCUS	CNS01A0A 540 bp mRNA PLN 02-SEP-1999
DEFINITION	<i>Botrytis cinerea</i> strain T4 cDNA library under conditions of nitrogen deprivation.
ACCESSION	AL113186
VERSION	AL113186.1 GI:5827805
KEYWORDS	cDNA library; nitrogen deprivation.
SOURCE	<i>Botrytislina fuckeliana</i> .
ORGANISM	<i>Botrytislina fuckeliana</i> Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE	1 (bases 1 to 540)
AUTHORS	Bilton,F., Levis,C., Fortin,D., Pradier,J.M. and Brygoo,Y.
TITLE	Direct Submission
JOURNAL	Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
REFERENCE	2 (bases 1 to 540)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
COMMENT	<p>- Web : www.genoscope.cns.fr</p> <p>The cDNA library to be analyzed within the framework of this project was created using a <i>Botrytis cinerea</i> strain which was grown under conditions of nitrogen deprivation, which is the normal</p>

/note="Genoscope sequence ID : W62D111"

Search completed: March 2, 2002, 20:57:16
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